

RAW SEQUENCE LISTING

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Application Serial Number: 10/024,019A
Source: IFW/6
Date Processed by STIC: 12/22/05

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IFW16

RAW SEQUENCE LISTING

DATE: 12/22/2005

PATENT APPLICATION: US/10/024,019A

TIME: 11:32:54

Input Set : A:\T154X.ST25.txt

Output Set: N:\CRF4\12222005\J024019A.raw

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3 <110> APPLICANT: Laughran, Thomas
4   Kothapalli, Ravi
6 <120> TITLE OF INVENTION: Sphingosine 1-Phosphate Receptor Gene, SPPR
8 <130> FILE REFERENCE: USF-T154X
10 <140> CURRENT APPLICATION NUMBER: US 10/024,019A
11 <141> CURRENT FILING DATE: 2001-12-21
13 <150> PRIOR APPLICATION NUMBER: US 60/257,119
14 <151> PRIOR FILING DATE: 2000-12-22
16 <160> NUMBER OF SEQ ID NOS: 19
18 <170> SOFTWARE: PatentIn version 3.3
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 17
22 <212> TYPE: DNA
23 <213> ORGANISM: Artificial Sequence
25 <220> FEATURE:
26 <223> OTHER INFORMATION: Probe (see p. 8 of specification)
28 <400> SEQUENCE: 1
29 gcgcggcccca tggagtc                                     17
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33 <211> LENGTH: 30
34 <212> TYPE: DNA
35 <213> ORGANISM: Artificial Sequence
37 <220> FEATURE:
38 <223> OTHER INFORMATION: Probe (see p. 8 of specification)
40 <400> SEQUENCE: 2
41 cttttctgtg ttcccaagca gaacgtcaat                         30
44 <210> SEQ ID NO: 3
45 <211> LENGTH: 398
46 <212> TYPE: PRT
47 <213> ORGANISM: Homo sapiens
50 <220> FEATURE:
51 <221> NAME/KEY: MISC_FEATURE
52 <223> OTHER INFORMATION: Human sphingosine 1-Phosphate receptor (SPPR) amino acid
sequence
53   (Figure 3)
55 <400> SEQUENCE: 3
57 Met Glu Ser Gly Leu Leu Arg Pro Ala Pro Val Ser Glu Val Ile Val
58 1           5           10           15
61 Leu His Tyr Asn Tyr Thr Gly Lys Leu Arg Gly Ala Arg Tyr Gln Pro
62           20           25           30
65 Gly Ala Gly Leu Arg Ala Asp Ala Val Val Cys Leu Ala Val Cys Ala
66           35           40           45
69 Phe Ile Val Leu Glu Asn Leu Ala Val Leu Leu Val Leu Gly Arg His
70           50           55           60

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73 Pro Arg Phe His Ala Pro Met Phe Leu Leu Leu Gly Ser Leu Thr Leu
74 65          70          75          80
77 Ser Asp Leu Leu Ala Gly Ala Ala Tyr Ala Ala Asn Ile Leu Leu Ser
78          85          90          95
81 Gly Pro Leu Thr Leu Lys Leu Ser Pro Ala Leu Trp Phe Ala Arg Glu
82          100         105         110
85 Gly Gly Val Phe Val Ala Leu Thr Ala Ser Val Leu Ser Leu Leu Ala
86          115         120         125
89 Ile Ala Leu Glu Arg Ser Leu Thr Met Ala Arg Arg Gly Pro Ala Pro
90          130         135         140
93 Val Ser Ser Arg Gly Arg Thr Leu Ala Met Ala Ala Ala Ala Trp Gly
94 145         150         155         160
97 Val Ser Leu Leu Leu Gly Leu Leu Pro Ala Leu Gly Trp Asn Cys Leu
98          165         170         175
101 Gly Arg Leu Asp Ala Cys Ser Thr Val Leu Pro Leu Tyr Ala Lys Ala
102          180         185         190
105 Tyr Val Leu Phe Cys Val Leu Ala Phe Val Gly Ile Leu Ala Ala Ile
106          195         200         205
109 Cys Ala Leu Tyr Ala Arg Ile Tyr Cys Gln Val Arg Ala Asn Ala Arg
110          210         215         220
113 Arg Leu Pro Ala Arg Pro Gly Thr Ala Gly Thr Thr Ser Thr Arg Ala
114 225         230         235         240
117 Arg Arg Lys Pro Arg Ser Leu Ala Leu Leu Arg Thr Leu Ser Val Val
118          245         250         255
121 Leu Leu Ala Phe Val Ala Cys Trp Gly Pro Leu Phe Leu Leu Leu Leu
122          260         265         270
125 Leu Asp Val Ala Cys Pro Ala Arg Thr Cys Pro Val Leu Leu Gln Ala
126          275         280         285
129 Asp Pro Phe Leu Gly Leu Ala Met Ala Asn Ser Leu Leu Asn Pro Ile
130          290         295         300
133 Ile Tyr Thr Leu Thr Asn Arg Asp Leu Arg His Ala Leu Leu Arg Leu
134 305         310         315         320
137 Val Cys Cys Gly Arg His Ser Cys Gly Arg Asp Pro Ser Gly Ser Gln
138          325         330         335
141 Gln Ser Ala Ser Ala Ala Glu Ala Ser Gly Gly Leu Arg Arg Cys Leu
142          340         345         350
145 Pro Pro Gly Leu Asp Gly Ser Phe Ser Gly Ser Glu Arg Ser Ser Pro
146          355         360         365
149 Gln Arg Asp Gly Leu Asp Thr Ser Gly Ser Thr Gly Ser Pro Gly Ala
150          370         375         380
153 Pro Thr Ala Ala Arg Thr Leu Val Ser Glu Pro Ala Ala Asp
154 385         390         395

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157 <210> SEQ ID NO: 4

158 <211> LENGTH: 2336

159 <212> TYPE: DNA

160 <213> ORGANISM: Homo sapiens

163 <220> FEATURE:

164 <221> NAME/KEY: MISC_FEATURE

165 <223> OTHER INFORMATION: Human sphingosine 1-Phosphate receptor (SPPR) cDNA sequence

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166 (Figure 3)

168 <400> SEQUENCE: 4

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169 gcgcggccca tggagtcggg gctgctgcgg ccggcgccgg tgagcgaggt catcgctctg      60
171 cattacaact acaccggcaa gctccgcggg gcgcgctacc agccgggtgc cggcctgcgc      120
173 gccgacgccg tgggtgtgct ggcggtgtgc gccttcacgc tgctagagaa tctagccgtg      180
175 ttgttggtgc tcggacgcca ccgcgccttc cacgctccca tgttctctgct cctgggcagc      240
177 ctcacgttgt cggatctgct ggcaggcgcc gcctacgcgc ccaacatcct actgtcgggg      300
179 ccgctcacgc tgaactgtc cccgcgcctc tggttcgcac gggagggagg cgtcttcgtg      360
181 gcactcactg cgtccgtgct gagcctcctg gccatcgcgc tggagcgagc cctcaccatg      420
183 gcgcgcaggg ggcccgcgcc cgtctccagt cgggggcgca cgctggcgat ggcagccgcg      480
185 gcctggggcg tgcgctgct cctcgggctc ctgccagcgc tgggctggaa ttgcctgggt      540
187 cgctggagc cttgctccac tgtcttgccg ctctacgcca aggcctacgt gctcttctgc      600
189 gtgctgcct tcgtgggcat cctggccgcg atctgtgcac tctacgcgcg catctactgc      660
191 caggtagcgc ccaacgcgcg gcgcctgccg gcacggcccc ggactgcggg gaccacctcg      720
193 acccgggcgc gtgcgaagcc gcgctcgctg gccttgcctg gcacgctcag cgtggtgctc      780
195 ctggcctttg tggcatgttg gggccccctc ttctgctgct tgttgcctga cgtggcgctg      840
197 ccggcgcgca cctgtcctgt actcctgcag gccgatccct tcttgggact ggccatggcc      900
199 aactcacttc tgaaccccat catctacacg ctcaccaacc gcgacctgcg ccacgcgctc      960
201 ctgcgccttg tctgctgcgg acgccactcc tgcggcagag acccgagtgg ctcccagcag      1020
203 tcggcgagcg cggctgaggg ttccgggggc ctgcgcgcgt gcctgcccc gggccttgat      1080
205 gggagcttca gcggctcgga gcgctcatcg ccccgagcgc acgggctgga caccagcggc      1140
207 tccacaggca gcccgggtgc acccacagcc gcccggactc tggtatcaga accggctgca      1200
209 gactgacacc ctgcgcccac gactgtcttc ccaagtttta cagacttggt ctttttacat      1260
211 aaaggaattt gtaggaaatg cagccaaagg tgcagtcgga aaagatgcag gggaaatgta      1320
213 tttatgcagc gacacccac aatgtgaaca aacagacaaa aaatctgtgc cctcgtggaa      1380
215 ttgacgttct gcttgggaac acagaaaaga actcgggtgat gaaataatgg agatgattcc      1440
217 agtgacaaac gacagagatg gtgatggtgg tcagggaaga cctctctgca gaggtagtga      1500
219 cttgtgatgt gagctgagac ctctgtcctg ggaagaccaa aagaaaagca tttcaggatg      1560
221 agggaatggc atgcgcaaag gccctgaggg tgaatgtgc ccatgtgttc taagaaatgc      1620
223 agcgatgctg gtgtgcctgg agcagggagc gagggggaga atgggaggag acaaggagct      1680
225 gaaggagtag ttcccgaagg accttgtggg tgatatagag gacttcgctt ttgctctgag      1740
227 tgagggtgga gccatagaag cttctaagca gaagagggac ttgccctaat tcaggatgat      1800
229 acagggtgtc tgtggcctcc atgggaggtt gaaaaccaca gaaggagaag gggggctgca      1860
231 ctgagccaca ggaacaatga tggagattcc agctaagccc agaccccgct gattctagat      1920
233 agattttaga ggcagcagac agaattactg aggaattgag tgtaagagtg gaataaagtt      1980
235 atcaaggaca atgccaaagg tggggcaccc ccaaatttga ctttgggaga ctacagccaaa      2040
237 tcctatctgg taataaaatt tcttttttat ttttcttttc tttctttctt tctttctttc      2100
239 tttttttttt tttgagttgg gatcttgtgc tctgtcaccc aggctggagt gcaatgggca      2160
241 caattatagc tactgcagc ctggaactcc tgggatcaag cctggagttc ctgcttcagc      2220
243 ctccctagta gctgggacta caggcatgca ccaccatgcc cagttaataa aatttcttca      2280
245 aatgcaaaaa aaaaaaaaaa aaaaaactcg agggggggcc cggtagccaa ttgcgc      2336

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248 <210> SEQ ID NO: 5

249 <211> LENGTH: 400

250 <212> TYPE: PRT

251 <213> ORGANISM: Rattus norvegicus

254 <220> FEATURE:

255 <221> NAME/KEY: MISC_FEATURE

256 <223> OTHER INFORMATION: Nrg-1 rat genes (Figure 4)

258 <400> SEQUENCE: 5

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260 Met Glu Ser Gly Leu Leu Arg Pro Ala Pro Val Ser Glu Val Ile Val
261 1 5 10 15
264 Leu His Tyr Asn Tyr Thr Gly Lys Leu Arg Gly Ala Arg Tyr Gln Pro
265 20 25 30
268 Gly Ala Gly Leu Arg Ala Asp Ala Ala Val Cys Leu Ala Val Cys Ala
269 35 40 45
272 Phe Ile Val Leu Glu Asn Leu Ala Val Leu Leu Val Leu Gly Arg His
273 50 55 60
276 Pro Arg Phe His Ala Pro Met Phe Leu Leu Leu Gly Ser Leu Thr Leu
277 65 70 75 80
280 Ser Asp Leu Leu Ala Gly Ala Ala Tyr Ala Thr Asn Ile Leu Leu Ser
281 85 90 95
284 Gly Pro Leu Thr Leu Arg Leu Ser Pro Ala Leu Trp Phe Ala Arg Glu
285 100 105 110
288 Gly Gly Val Phe Val Ala Leu Ala Ser Val Leu Ser Leu Leu Ala
289 115 120 125
292 Ile Ala Ile Glu Arg His Leu Thr Met Ala Arg Arg Gly Pro Ala Pro
293 130 135 140
296 Ala Ala Ser Arg Ala Arg Thr Leu Ala Met Ala Val Ala Ala Trp Gly
297 145 150 155 160
300 Leu Leu Leu Thr Leu Gly Leu Leu Pro Ala Leu Gly Trp Asn Cys Leu
301 165 170 175
304 Gly Arg Leu Glu Ala Cys Ser Thr Val Leu Pro Val Tyr Ala Lys Ala
305 180 185 190
308 Tyr Val Leu Phe Cys Val Leu Ala Phe Leu Gly Ile Leu Ala Ala Ile
309 195 200 205
312 Cys Ala Leu Tyr Ala Arg Ile Tyr Cys Gln Val Arg Ala Asn Ala Arg
313 210 215 220
316 Arg Leu Arg Ala Gly Pro Gly Ser Arg Arg Ala Thr Ser Ser Ser Arg
317 225 230 235 240
320 Ser Arg His Thr Pro Arg Ser Leu Ala Leu Leu Arg Thr Leu Ser Val
321 245 250 255
324 Val Leu Leu Ala Phe Val Ala Cys Trp Gly Pro Leu Phe Leu Leu Leu
325 260 265 270
328 Leu Leu Asp Val Ala Cys Pro Ala Arg Ala Cys Pro Val Leu Leu Gln
329 275 280 285
332 Ala Asp Pro Phe Leu Gly Leu Ala Met Ala Asn Ser Leu Leu Asn Pro
333 290 295 300
336 Ile Ile Tyr Thr Phe Thr Asn Arg Asp Leu Arg His Ala Leu Leu Arg
337 305 310 315 320
340 Leu Leu Cys Cys Gly Arg Gly Pro Cys Asn Gln Asp Ser Ser Asn Ser
341 325 330 335
344 Leu Gln Arg Ser Pro Ser Ala Val Gly Pro Ser Gly Gly Gly Leu Arg
345 340 345 350
348 Arg Cys Leu Pro Pro Thr Leu Asp Arg Ser Ser Ser Pro Ser Glu His
349 355 360 365
352 Ser Cys Pro Gln Arg Asp Gly Met Asp Thr Ser Cys Ser Thr Gly Ser
353 370 375 380
356 Pro Gly Ala Ala Thr Ala Asn Arg Thr Leu Val Pro Asp Ala Thr Asp

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361 <211> LENGTH: 400
362 <212> TYPE: PRT
363 <213> ORGANISM: Rattus norvegicus
366 <220> FEATURE:
367 <221> NAME/KEY: MISC_FEATURE
368 <223> OTHER INFORMATION: EDG-8 rat genes (Figure 4)
370 <400> SEQUENCE: 6
372 Met Glu Ser Gly Leu Leu Arg Pro Ala Pro Val Ser Glu Val Ile Val
373 1          5          10          15
376 Leu His Tyr Asn Tyr Thr Gly Lys Leu Arg Gly Ala Arg Tyr Gln Pro
377          20          25          30
380 Gly Ala Gly Leu Arg Ala Asp Ala Ala Val Cys Leu Ala Val Cys Ala
381          35          40          45
384 Phe Ile Val Leu Glu Asn Leu Ala Val Leu Leu Val Leu Gly Arg His
385          50          55          60
388 Pro Arg Phe His Ala Pro Met Phe Leu Leu Leu Gly Ser Leu Thr Leu
389 65          70          75          80
392 Ser Asp Leu Leu Ala Gly Ala Ala Tyr Ala Thr Asn Ile Leu Leu Ser
393          85          90          95
396 Gly Pro Leu Thr Leu Arg Leu Ser Pro Ala Leu Trp Phe Ala Arg Glu
397          100         105         110
400 Gly Gly Val Phe Val Ala Leu Ala Ala Ser Val Leu Ser Leu Leu Ala
401          115         120         125
404 Ile Ala Leu Glu Arg His Leu Thr Met Ala Arg Arg Gly Pro Ala Pro
405          130         135         140
408 Ala Ala Ser Arg Ala Arg Thr Leu Ala Met Ala Val Ala Ala Trp Gly
409 145         150         155         160
412 Leu Ser Leu Leu Leu Gly Leu Leu Pro Ala Leu Gly Trp Asn Cys Leu
413          165         170         175
416 Gly Arg Leu Glu Ala Cys Ser Thr Val Leu Pro Leu Tyr Ala Lys Ala
417          180         185         190
420 Tyr Val Leu Phe Cys Val Leu Ala Phe Leu Gly Ile Leu Ala Ala Ile
421          195         200         205
424 Cys Ala Leu Tyr Ala Arg Ile Tyr Cys Gln Val Arg Ala Asn Ala Arg
425          210         215         220
428 Arg Leu Arg Ala Gly Pro Gly Ser Arg Arg Ala Thr Ser Ser Ser Arg
429 225         230         235         240
432 Ser Arg His Thr Pro Arg Ser Leu Ala Leu Leu Arg Thr Leu Ser Val
433          245         250         255
436 Val Leu Leu Ala Phe Val Ala Cys Trp Gly Pro Leu Phe Leu Leu Leu
437          260         265         270
440 Leu Leu Asp Val Ala Cys Pro Ala Arg Ala Cys Pro Val Leu Leu Gln
441          275         280         285
444 Ala Asp Pro Phe Leu Gly Leu Ala Met Ala Asn Ser Leu Leu Asn Pro
445          290         295         300
448 Ile Ile Tyr Thr Phe Thr Asn Arg Asp Leu Arg His Ala Leu Leu Arg
449 305         310         315         320

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VERIFICATION SUMMARY

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